

## SEQUENCE LISTING

<110> Piddington, Christopher S.  
Bishop, Paul D.

<120> ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG  
ZACRP2

<130> 99-08D1

<150> US 09/552,204

<151> 2000-04-19

<150> US 60/130,207

<151> 1999-04-20

<160> 23

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1161

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (133)...(987)

<400> 1

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gcggagcccc gccgagagct tctttgctcc ggacgcccct ggacgtggcg ggcagccgcg 120
agggtaacca cc atg atc ccc tgg gtg ctc ctg gcc tgt gcc ctc ccc tgt 171
          Met Ile Pro Trp Val Leu Leu Ala Cys Ala Leu Pro Cys
                1             5             10

gct gct gac cca ctg ctt ggc gcc ttt gct cgc agg gac ttc cgg aaa 219
Ala Ala Asp Pro Leu Leu Gly Ala Phe Ala Arg Arg Asp Phe Arg Lys
      15             20             25

ggc tcc cct caa ctg gtc tgc agc ctg cct ggc ccc cag ggc cca ccc 267
Gly Ser Pro Gln Leu Val Cys Ser Leu Pro Gly Pro Gln Gly Pro Pro
      30             35             40             45

ggc ccc cca gga gcc cca ggg ccc tca gga atg atg gga cga atg ggc 315
Gly Pro Pro Gly Ala Pro Gly Pro Ser Gly Met Met Gly Arg Met Gly
                50             55             60

ttt cct ggc aaa gac ggc caa gat gga cac gac ggc gac cgg ggg gac 363
Phe Pro Gly Lys Asp Gly Gln Asp Gly His Asp Gly Asp Arg Gly Asp
                65             70             75

agc gga gag gaa ggt cca cct ggc cgg aca ggt aac cgg gga aag cca 411
Ser Gly Glu Glu Gly Pro Pro Gly Arg Thr Gly Asn Arg Gly Lys Pro
      80             85             90

gga cca aag ggc aaa gcc ggg gcc att ggg cgg gct ggc ccc cgt ggc 459
Gly Pro Lys Gly Lys Ala Gly Ala Ile Gly Arg Ala Gly Pro Arg Gly
      95             100             105

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ccc aag ggg gtc aac ggt acc ccc ggg aag cat ggc aca cca ggc aag 507
Pro Lys Gly Val Asn Gly Thr Pro Gly Lys His Gly Thr Pro Gly Lys
110                               115                               120                               125

aag ggg ccc aag ggc aag aaa ggg gag cca ggc ctc cca ggc ccc tgc 555
Lys Gly Pro Lys Gly Lys Lys Gly Glu Pro Gly Leu Pro Gly Pro Cys
                               130                               135                               140

agc tgt ggc agt ggc cat acc aag tca gct ttc tcg gtg gca gtg acc 603
Ser Cys Gly Ser Gly His Thr Lys Ser Ala Phe Ser Val Ala Val Thr
                               145                               150                               155

aag agc tac cca cgg gag cgg ctg ccc atc aag ttt gac aag att ctg 651
Lys Ser Tyr Pro Arg Glu Arg Leu Pro Ile Lys Phe Asp Lys Ile Leu
                               160                               165                               170

atg aac gag ggt ggc cac tac aat gct tcc agc ggc aag ttc gtc tgc 699
Met Asn Glu Gly Gly His Tyr Asn Ala Ser Ser Gly Lys Phe Val Cys
                               175                               180                               185

ggc gtg cct ggg atc tac tac ttc acc tac gac atc acg ctg gcc aac 747
Gly Val Pro Gly Ile Tyr Tyr Phe Thr Tyr Asp Ile Thr Leu Ala Asn
190                               195                               200                               205

aag cac ctg gcc atc ggc ctg gtg cac aac ggc cag tac cgc atc cgg 795
Lys His Leu Ala Ile Gly Leu Val His Asn Gly Gln Tyr Arg Ile Arg
                               210                               215                               220

acc ttt gat gcc aac acc ggc aac cac gat gtg gcc tca ggc tcc acc 843
Thr Phe Asp Ala Asn Thr Gly Asn His Asp Val Ala Ser Gly Ser Thr
                               225                               230                               235

atc ctg gct ctc aag cag ggt gac gaa gtt tgg ctg cag atc ttc tac 891
Ile Leu Ala Leu Lys Gln Gly Asp Glu Val Trp Leu Gln Ile Phe Tyr
                               240                               245                               250

tca gag cag aac ggg ctc ttc tat gac cct tac tgg aca gac agc ctc 939
Ser Glu Gln Asn Gly Leu Phe Tyr Asp Pro Tyr Trp Thr Asp Ser Leu
                               255                               260                               265

ttt acg ggc ttc cta atc tat gcc gac cag gat gac ccc aac gag gta 987
Phe Thr Gly Phe Leu Ile Tyr Ala Asp Gln Asp Asp Pro Asn Glu Val
270                               275                               280                               285

tagacatgcc acggcgggtcc tccaggcagg gaacaagctt ctggacttgg gcttacagag 1047
caagacccca caactgtagg ctgggggtgg ggggtcgagt gagcggttct agcctcaggc 1107
tcacctcctc cgctcttttt tttcccttcc attaaatcca aaccttttta ttca 1161

<210> 2
<211> 285
<212> PRT
<213> Homo sapiens

<400> 2
Met Ile Pro Trp Val Leu Leu Ala Cys Ala Leu Pro Cys Ala Ala Asp
1 5 10 15
Pro Leu Leu Gly Ala Phe Ala Arg Arg Asp Phe Arg Lys Gly Ser Pro
20 25 30
Gln Leu Val Cys Ser Leu Pro Gly Pro Gln Gly Pro Pro Gly Pro Pro
35 40 45
Gly Ala Pro Gly Pro Ser Gly Met Met Gly Arg Met Gly Phe Pro Gly

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50 55 60  
 Lys Asp Gly Gln Asp Gly His Asp Gly Asp Arg Gly Asp Ser Gly Glu  
 65 70 75 80  
 Glu Gly Pro Pro Gly Arg Thr Gly Asn Arg Gly Lys Pro Gly Pro Lys  
 85 90 95  
 Gly Lys Ala Gly Ala Ile Gly Arg Ala Gly Pro Arg Gly Pro Lys Gly  
 100 105 110  
 Val Asn Gly Thr Pro Gly Lys His Gly Thr Pro Gly Lys Lys Gly Pro  
 115 120 125  
 Lys Gly Lys Lys Gly Glu Pro Gly Leu Pro Gly Pro Cys Ser Cys Gly  
 130 135 140  
 Ser Gly His Thr Lys Ser Ala Phe Ser Val Ala Val Thr Lys Ser Tyr  
 145 150 155 160  
 Pro Arg Glu Arg Leu Pro Ile Lys Phe Asp Lys Ile Leu Met Asn Glu  
 165 170 175  
 Gly Gly His Tyr Asn Ala Ser Ser Gly Lys Phe Val Cys Gly Val Pro  
 180 185 190  
 Gly Ile Tyr Tyr Phe Thr Tyr Asp Ile Thr Leu Ala Asn Lys His Leu  
 195 200 205  
 Ala Ile Gly Leu Val His Asn Gly Gln Tyr Arg Ile Arg Thr Phe Asp  
 210 215 220  
 Ala Asn Thr Gly Asn His Asp Val Ala Ser Gly Ser Thr Ile Leu Ala  
 225 230 235 240  
 Leu Lys Gln Gly Asp Glu Val Trp Leu Gln Ile Phe Tyr Ser Glu Gln  
 245 250 255  
 Asn Gly Leu Phe Tyr Asp Pro Tyr Trp Thr Asp Ser Leu Phe Thr Gly  
 260 265 270  
 Phe Leu Ile Tyr Ala Asp Gln Asp Asp Pro Asn Glu Val  
 275 280 285

<210> 3  
 <211> 244  
 <212> PRT  
 <213> Homo sapiens

<400> 3  
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 1 5 10 15  
 Asp Gln Glu Thr Thr Thr Gln Gly Pro Gly Val Leu Leu Pro Leu Pro  
 20 25 30  
 Lys Gly Ala Cys Thr Gly Trp Met Ala Gly Ile Pro Gly His Pro Gly  
 35 40 45  
 His Asn Gly Ala Pro Gly Arg Asp Gly Arg Asp Gly Thr Pro Gly Glu  
 50 55 60  
 Lys Gly Glu Lys Gly Asp Pro Gly Leu Ile Gly Pro Lys Gly Asp Ile  
 65 70 75 80  
 Gly Glu Thr Gly Val Pro Gly Ala Glu Gly Pro Arg Gly Phe Pro Gly  
 85 90 95  
 Ile Gln Gly Arg Lys Gly Glu Pro Gly Glu Gly Ala Tyr Val Tyr Arg  
 100 105 110  
 Ser Ala Phe Ser Val Gly Leu Glu Thr Tyr Val Thr Ile Pro Asn Met  
 115 120 125  
 Pro Ile Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn His Tyr Asp  
 130 135 140  
 Gly Ser Thr Gly Lys Phe His Cys Asn Ile Pro Gly Leu Tyr Tyr Phe  
 145 150 155 160  
 Ala Tyr His Ile Thr Val Tyr Met Lys Asp Val Lys Val Ser Leu Phe  
 165 170 175  
 Lys Lys Asp Lys Ala Met Leu Phe Thr Tyr Asp Gln Tyr Gln Glu Asn  
 180 185 190

Asn Val Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu Glu Val Gly  
                   195                  200                  205  
 Asp Gln Val Trp Leu Gln Val Tyr Gly Glu Gly Glu Arg Asn Gly Leu  
           210                  215                  220  
 Tyr Ala Asp Asn Asp Asn Asp Ser Thr Phe Thr Gly Phe Leu Leu Tyr  
   225                  230                  235                  240  
 His Asp Thr Asn

<210> 4  
 <211> 245  
 <212> PRT  
 <213> Homo sapiens

<400> 4  
 Met Asp Val Gly Pro Ser Ser Leu Pro His Leu Gly Leu Lys Leu Leu  
   1                  5                  10                  15  
 Leu Leu Leu Leu Leu Leu Ala Leu Arg Gly Gln Ala Asn Thr Gly Cys  
           20                  25                  30  
 Tyr Gly Ile Pro Gly Met Pro Gly Leu Pro Gly Ala Pro Gly Lys Asp  
           35                  40                  45  
 Gly Tyr Asp Gly Leu Pro Gly Pro Lys Gly Glu Pro Gly Ile Pro Ala  
   50                  55                  60  
 Ile Pro Gly Ile Arg Gly Pro Lys Gly Gln Lys Gly Glu Pro Gly Leu  
  65                  70                  75                  80  
 Pro Gly His Pro Gly Lys Asn Gly Pro Met Gly Pro Pro Gly Met Pro  
           85                  90                  95  
 Gly Val Pro Gly Pro Met Gly Ile Pro Gly Glu Pro Gly Glu Gly  
          100                 105                 110  
 Arg Tyr Lys Gln Lys Phe Gln Ser Val Phe Thr Val Thr Arg Gln Thr  
          115                 120                 125  
 His Gln Pro Pro Ala Pro Asn Ser Leu Ile Arg Phe Asn Ala Val Leu  
  130                 135                 140  
 Thr Asn Pro Gln Gly Asp Tyr Asp Thr Ser Thr Gly Lys Phe Thr Cys  
  145                 150                 155                 160  
 Lys Val Pro Gly Leu Tyr Tyr Phe Val Tyr His Ala Ser His Thr Ala  
          165                 170                 175  
 Asn Leu Cys Val Leu Leu Tyr Arg Ser Gly Val Lys Val Val Thr Phe  
          180                 185                 190  
 Cys Gly His Thr Ser Lys Thr Asn Gln Val Asn Ser Gly Gly Val Leu  
          195                 200                 205  
 Leu Arg Leu Gln Val Gly Glu Glu Val Trp Leu Ala Val Asn Asp Tyr  
  210                 215                 220  
 Tyr Asp Met Val Gly Ile Gln Gly Ser Asp Ser Val Phe Ser Gly Phe  
  225                 230                 235                 240  
 Leu Leu Phe Pro Asp  
                   245

<210> 5  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Aromatic motif

<221> VARIANT  
 <222> (2)...(6)  
 <223> Each Xaa is independently any amino acid residue.

<221> VARIANT  
 <222> (7)...(7)  
 <223> Xaa is asparagine or aspartic acid.

<221> VARIANT  
 <222> (8)...(11)  
 <223> Each Xaa is independently any amino acid residue.

<221> VARIANT  
 <222> (12)...(12)  
 <223> Xaa is phenyalanine, tyrosine, tryptophan or leucine.

<221> VARIANT  
 <222> (13)...(18)  
 <223> Each Xaa is independently any amino acid residue.

<221> VARIANT  
 <222> (20)...(24)  
 <223> Each Xaa is independently any amino acid residue.

<221> VARIANT  
 <222> (26)...(26)  
 <223> Xaa is any amino acid residue.

<221> VARIANT  
 <222> (28)...(28)  
 <223> Xaa is any amino acid residue.

<221> VARIANT  
 <222> (30)...(30)  
 <223> Xaa is any amino acid residue.

<221> VARIANT  
 <222> (31)...(31)  
 <223> Xaa is phenyalanine or tyrosine.

<400> 5  
 Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 1 5 10 15  
 Xaa Xaa Phe Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Phe Xaa Xaa  
 20 25 30

<210> 6  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Degenerate nucleotide primer

<221> variation  
 <222> (1)...(17)  
 <223> n = A, T, G or C

<400> 6  
 ggngansarg tntggyt

<210> 7

<211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Degenerate nucleotide primer

<221> variation  
 <222> (1)...(18)  
 <223> n = A, T, G or C

<400> 7  
 snggnntnta ytwytttyr 18

<210> 8  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Degenerate nucleotide primer

<221> variation  
 <222> (1)...(17)  
 <223> n = A, T, G or C

<400> 8  
 ttydsnggnt tyytnht 17

<210> 9  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Degenerate nucleotide primer

<221> variation  
 <222> (1)...(18)  
 <223> n = A, T, G or C

<400> 9  
 ytwyrayrbn wbnwsngg 18

<210> 10  
 <211> 855  
 <212> DNA  
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 <223> Degenerate nucleotide sequence encoding the  
 polypeptide of SEQ ID NO:2.

<221> variation  
 <222> (1)...(855)  
 <223> n = A, T, G or C

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 atgathccnt gggtnytnyt ngcntgygcn ytnccntgyg cngcngaycc nytnytnngn 60  
 gcnttygcnm gnmngaytt ymgnaarggn wsnccncary tngtntgyws nytnccnggn 120

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ccncarggnc cncnggncc nccngngncn ccnggnccnw snggnatgat gggnmgnatg 180
ggnttyccng gnaargaygg ncargayggg caygayggng aymngngnga ywsngnggar 240
garggnccnc cnggnmgnac nggnaaymgn ggnaarccng gncnaargg naargcnggn 300
gcnathggnm gngcnggncc nmngngnccn aargngtna ayggnaacnc nggnaarcay 360
ggnacnccng gnaaraargg nccnaarggn aaraarggng arccnggnyt nccnggnccn 420
tgywsntgyg gnwsnggnca yacnaarwsn gcnttywsng tngcngtnac naarwsntay 480
ccnmnggarm gnytnccnat haarttygay aarathytna tgaaygargg nggncaytay 540
aaygcwnsnw snggnaartt ygtntgyggg gtncnggna thtaytaytt yacntaygay 600
athacnytn gnaayaarca yytngcnath ggnytngtnc ayaayggna rtaymgnath 660
mgnacnttyg aygcnaayac nggnaaycay gaygtngcnw snggnwsnac nathytnngcn 720
ytnaarcarg gngaygargt ntggytncar athtitytayw sngarcaraa yggnytnnty 780
taygayccnt aytggacnga ywsnytnnty acnggnttyy tnathtaygc ngaycargay 840
gayccnaayg argtn 855

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<210> 11
<211> 536
<212> DNA
<213> Mus musculus

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<220>
<221> CDS
<222> (1)...(360)

<221> variation
<222> (1)...(536)
<223> n = A, T, G or C

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<400> 11
atc aag ttt gac aag att ctg atg aac gag ggt ggc cac tac aac gcg 48
Ile Lys Phe Asp Lys Ile Leu Met Asn Glu Gly Gly His Tyr Asn Ala
1 5 10 15

tcc agt ggc aag ttc gtc tgc agc gtg ccg ggg atc tna tta cnt tta 96
Ser Ser Gly Lys Phe Val Cys Ser Val Pro Gly Ile Xaa Leu Xaa Leu
20 25 30

cct atg aca tta cgc ntg gcc aac aaa cac ctg gnc atc ggc ctg gtg 144
Pro Met Thr Leu Arg Xaa Ala Asn Lys His Leu Xaa Ile Gly Leu Val
35 40 45

cac aat ggt cag tac cgc att cgg act ttt gat gcc aac acg ggc aac 192
His Asn Gly Gln Tyr Arg Ile Arg Thr Phe Asp Ala Asn Thr Gly Asn
50 55 60

cac gac gtg gcc tcg ggc tcc acc atc cta gct ctc aag gag ggt gat 240
His Asp Val Ala Ser Gly Ser Thr Ile Leu Ala Leu Lys Glu Gly Asp
65 70 75 80

gaa gtc tgg ctg cag atc ttc tac tca gag cag aat ggc ctc ttc tac 288
Glu Val Trp Leu Gln Ile Phe Tyr Ser Glu Gln Asn Gly Leu Phe Tyr
85 90 95

gac cct tac tgg acc gac agc ctg ttc acc ggc ttc ctc atc tac gct 336
Asp Pro Tyr Trp Thr Asp Ser Leu Phe Thr Gly Phe Leu Ile Tyr Ala
100 105 110

gac caa gga gac ccc aac gag gta tagacaagcc ggggttgagc cttgaggtag 390
Asp Gln Gly Asp Pro Asn Glu Val
115 120

ggactaagag tctgcgtggg tgcctggagg aagatccctc gactggggct gtggactgac 450

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ttaaataccaa gctattgatt catcta 536

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<211> 120  
<212> PRT  
<213> Mus musculus

<220>  
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<222> 29  
<223> Xaa is any amino acid

<221> VARIANT  
<222> 31  
<223> Xaa is any amino acid

<221> VARIANT  
<222> 38  
<223> Xaa is any amino acid

<221> VARIANT  
<222> 44  
<223> Xaa is any amino acid

<400> 12  
Ile Lys Phe Asp Lys Ile Leu Met Asn Glu Gly Gly His Tyr Asn Ala  
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Ser Ser Gly Lys Phe Val Cys Ser Val Pro Gly Ile Xaa Leu Xaa Leu  
20 25 30  
Pro Met Thr Leu Arg Xaa Ala Asn Lys His Leu Xaa Ile Gly Leu Val  
35 40 45  
His Asn Gly Gln Tyr Arg Ile Arg Thr Phe Asp Ala Asn Thr Gly Asn  
50 55 60  
His Asp Val Ala Ser Gly Ser Thr Ile Leu Ala Leu Lys Glu Gly Asp  
65 70 75 80  
Glu Val Trp Leu Gln Ile Phe Tyr Ser Glu Gln Asn Gly Leu Phe Tyr  
85 90 95  
Asp Pro Tyr Trp Thr Asp Ser Leu Phe Thr Gly Phe Leu Ile Tyr Ala  
100 105 110  
Asp Gln Gly Asp Pro Asn Glu Val  
115 120

<210> 13  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide ZC20810

<400> 13  
gggcttccta atctatgc

18

<210> 14  
<211> 18  
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<213> Artificial Sequence  
  
<220>



<223> Oligonucleotide ZC20809  
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 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Oligonucleotide ZC23375  
 <400> 15  
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 <210> 16  
 <211> 23  
 <212> DNA  
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 <400> 16  
 gccgtggtct agatatacct cgt 23  
 <210> 17  
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 <223> Glu-Glu tag  
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 Glu Glu Tyr Met Pro Met Glu  
 1 5  
 <210> 18  
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 <400> 18  
 taacaatttc acacagg 17  
 <210> 19  
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 <212> DNA  
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cgttgtaaaa cgacggcc 18

<210> 20  
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 <212> PRT  
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<220>  
 <223> purification peptide

<400> 20  
 Glu Tyr Met Pro Val Asp  
 1 5

<210> 21  
 <211> 12  
 <212> DNA  
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<220>  
 <223> Representative contig

<400> 21  
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<210> 22  
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<220>  
 <223> Representative contig

<400> 22  
 tagcttgagt ct 12

<210> 23  
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<220>  
 <223> Representative contig

<400> 23  
 agccatcagc tg 12